



FIG. 1

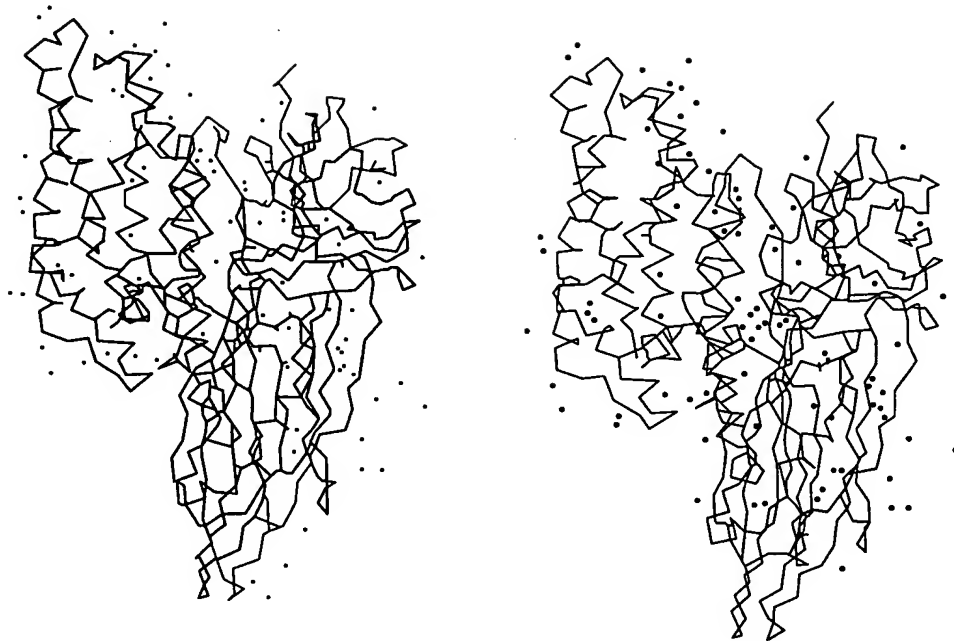


FIG. 2

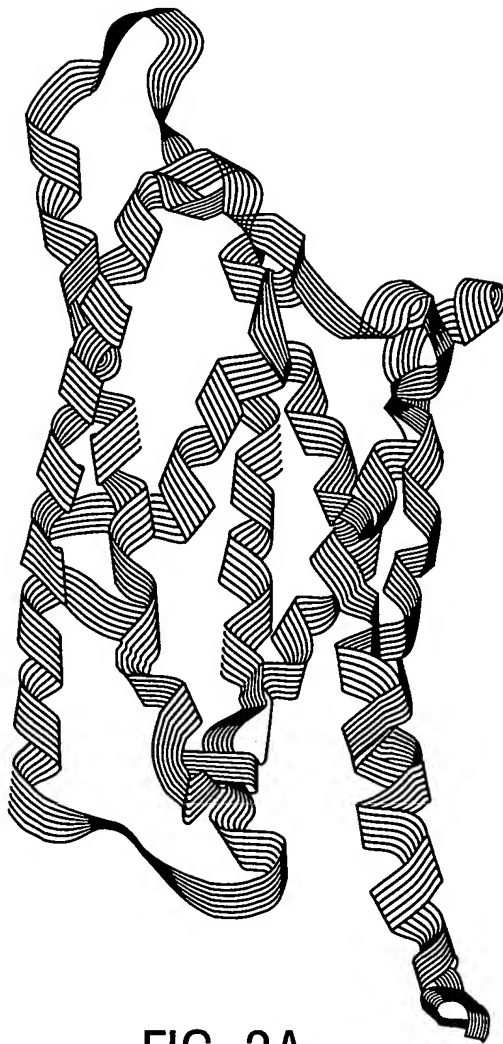


FIG. 3A

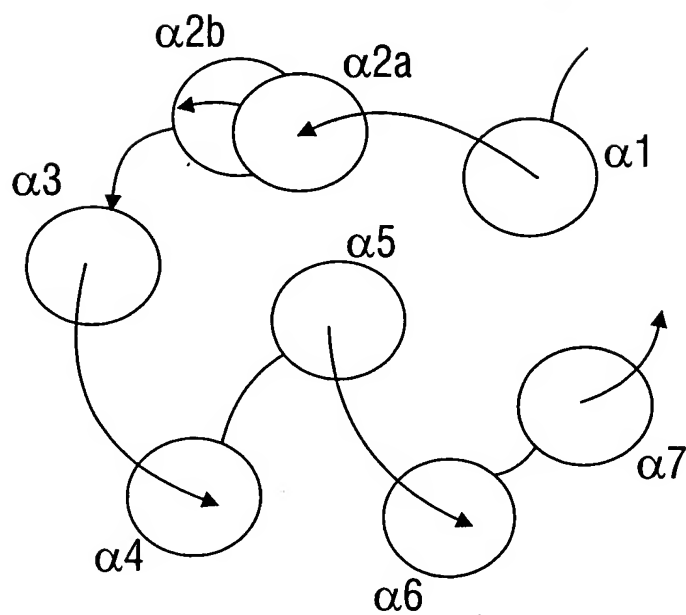


FIG. 3B

alpha helix	Amino acid Residues
$\alpha 1$	63-79
$\alpha 2a$	85-98
$\alpha 2b$	105-118
$\alpha 3$	124-153
$\alpha 4$	161-186
$\alpha 5$	194-215
$\alpha 6$	223-255
$\alpha 7$	260-286

FIG. 4

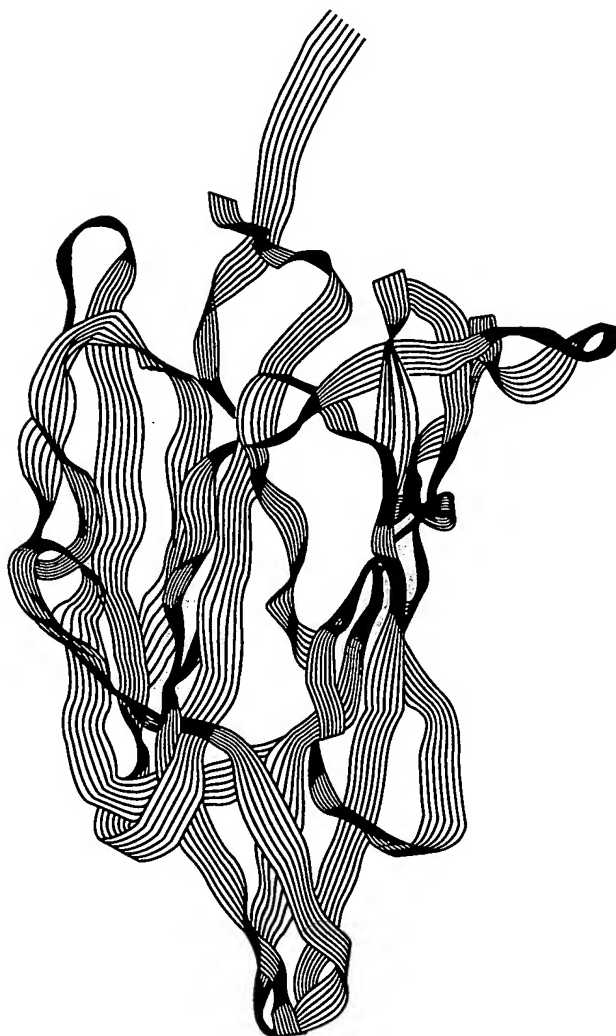


FIG. 5A

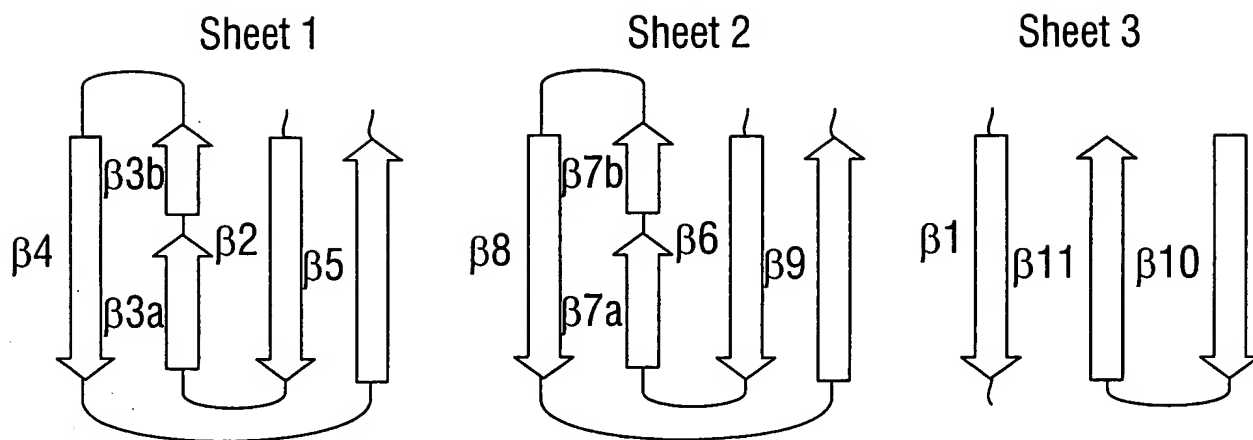


FIG. 5B

Sheet 1

β Strand	Amino Acid Residue
$\beta 2$	339-350
$\beta 3a$	256-360
$\beta 3b$	362-368
$\beta 4$	375-379
$\beta 5$	390-395

Sheet 2

β Strand	Amino Acid Residue
$\beta 6$	402-412
$\beta 7a$	416-419
$\beta 7b$	423-430
$\beta 8$	435-442
$\beta 9$	452-456

Sheet 3

β Strand	Amino Acid Residue
$\beta 1$	296-306
$\beta 10$	472-483
$\beta 11$	492-498

FIG. 6

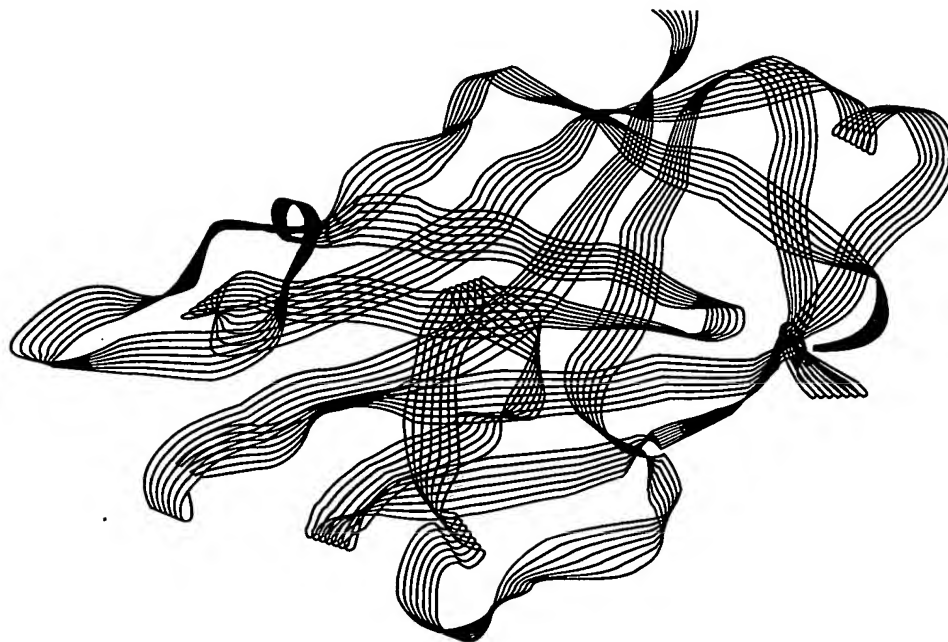


FIG. 7A

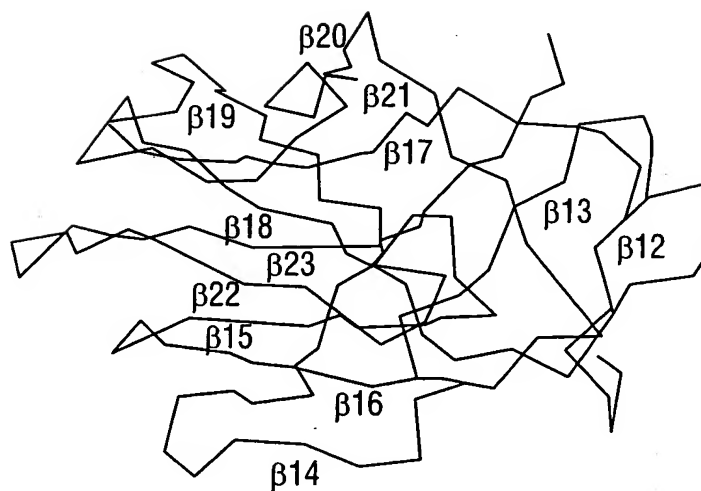


FIG. 7B

Strand Number	Amino Acid Residues
β 12	505-509
β 13	512-515
β 14	522-528
β 15	539-544
β 16	550-557
β 17	563-574
β 18	578-584
β 19	590-596
β 20	609-614
β 21	616-619
β 22	626-636
β 23	638-650

FIG. 8



FIG. 9A

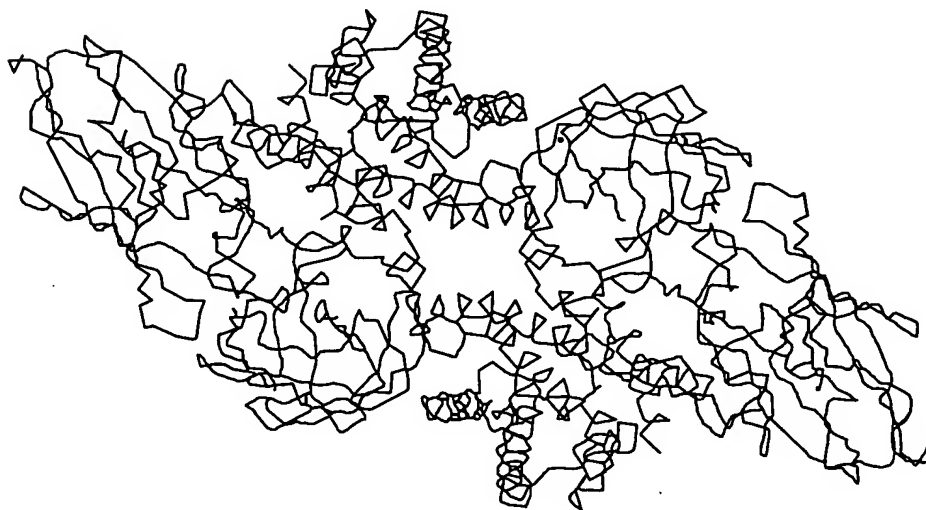


FIG. 9B

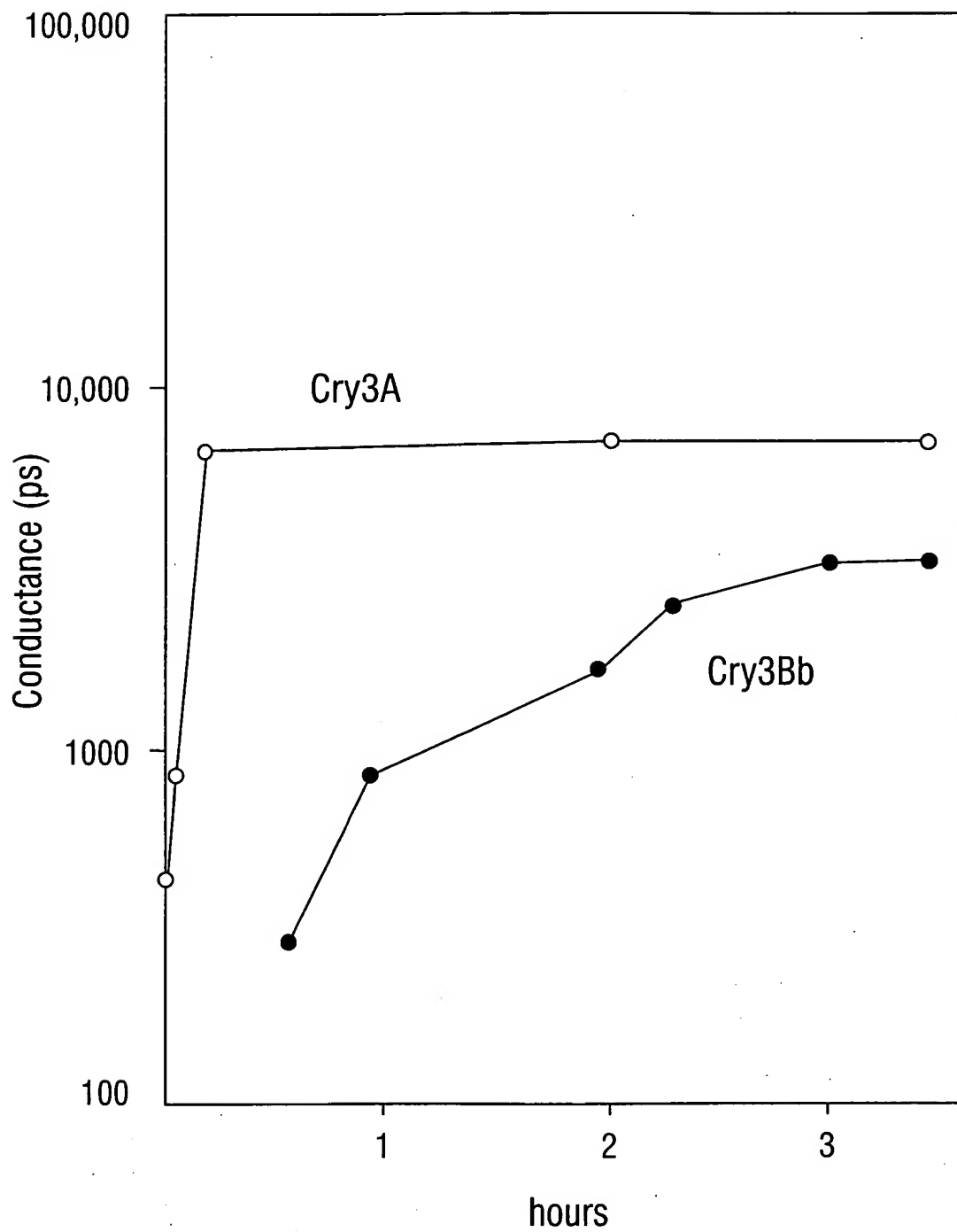


FIG. 10

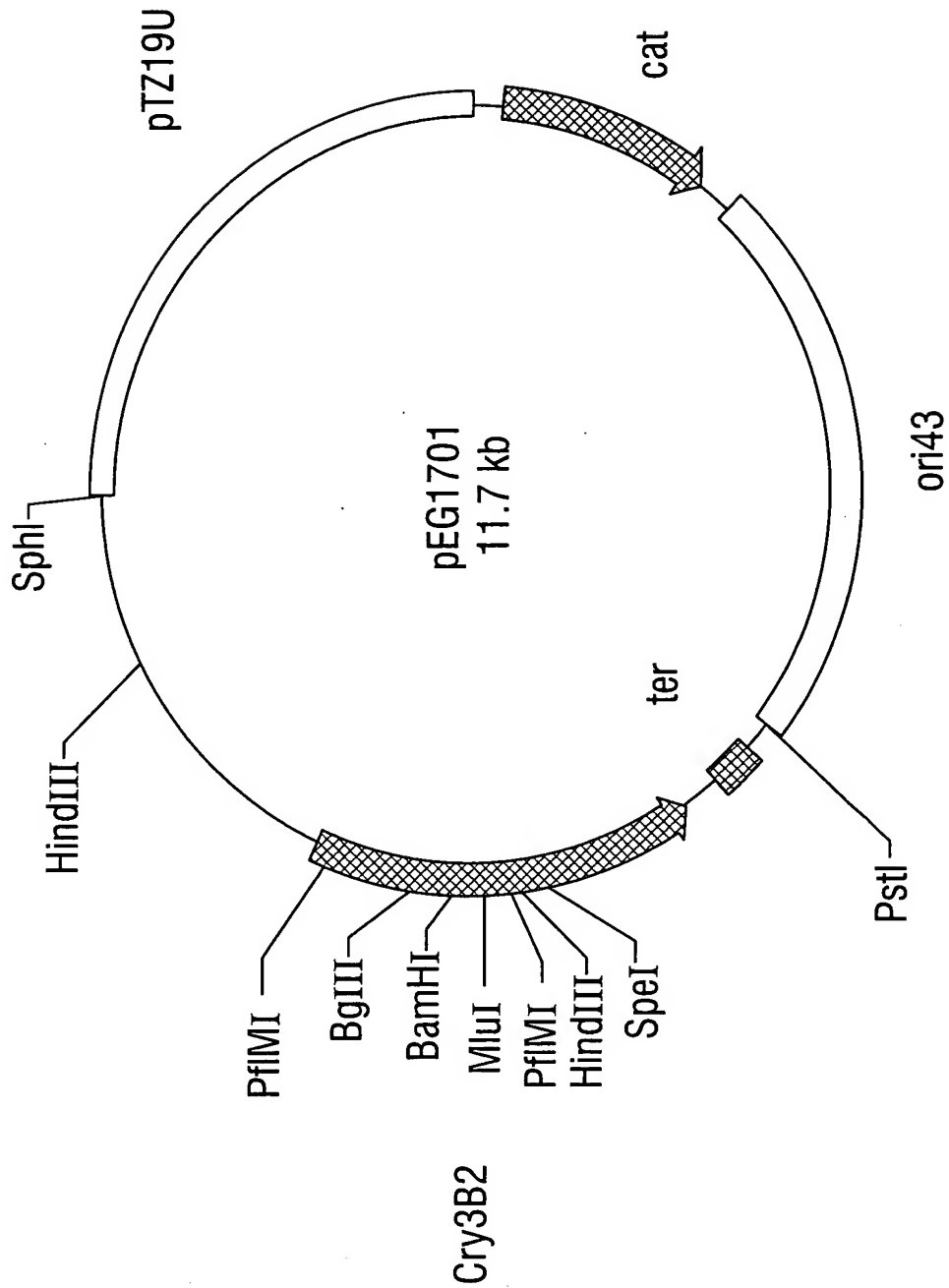


FIG. 11

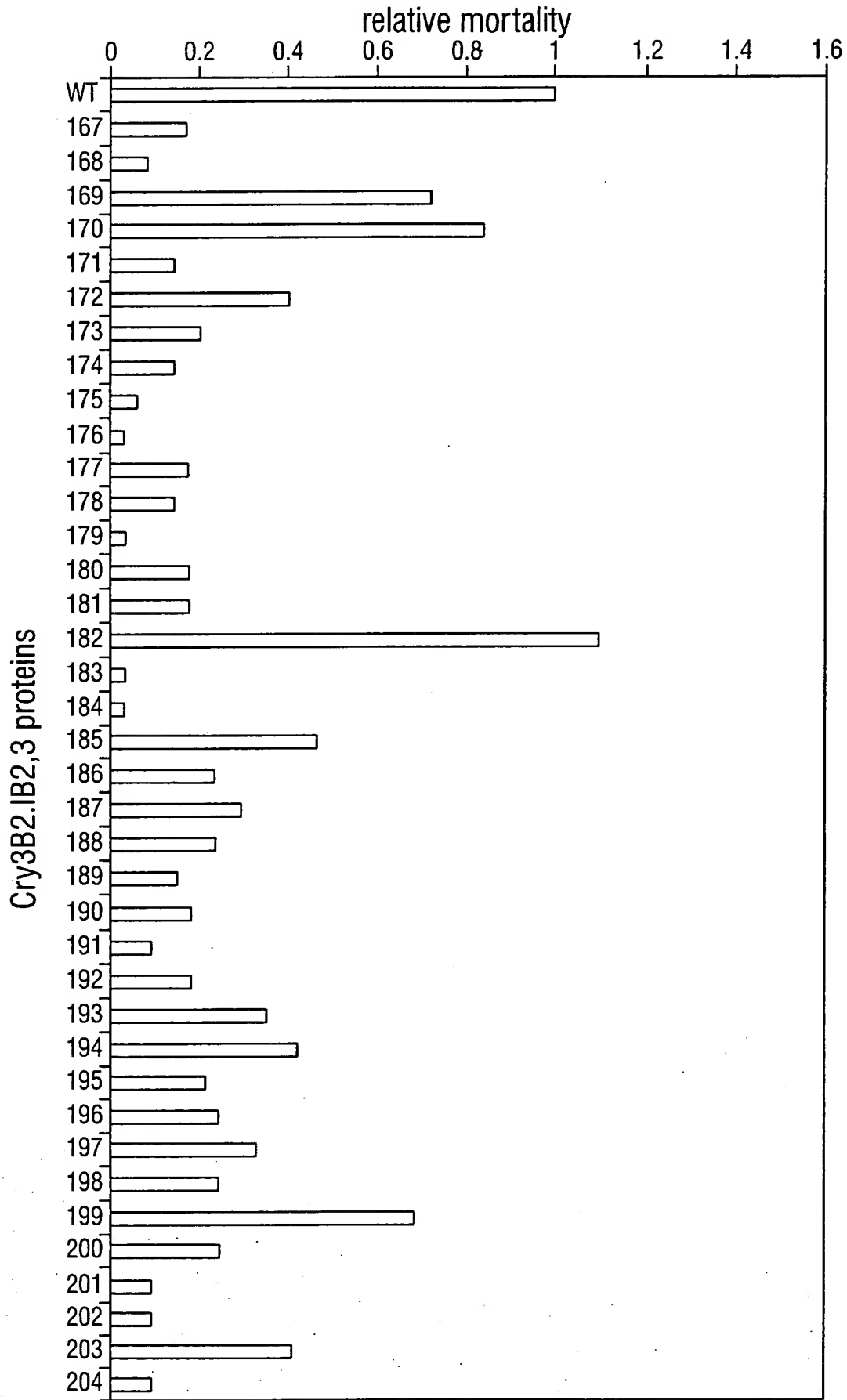


FIG. 12

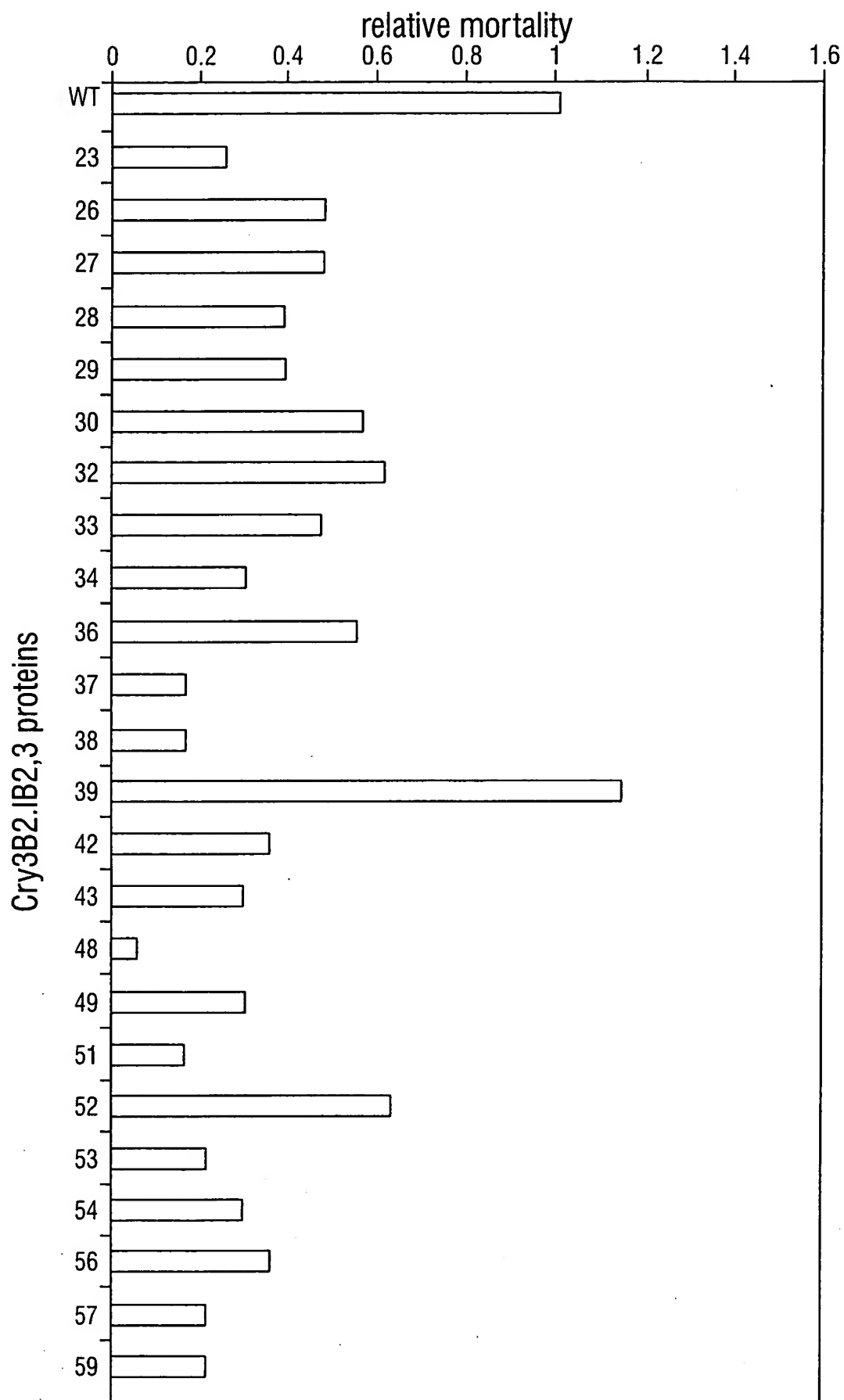


FIG. 13

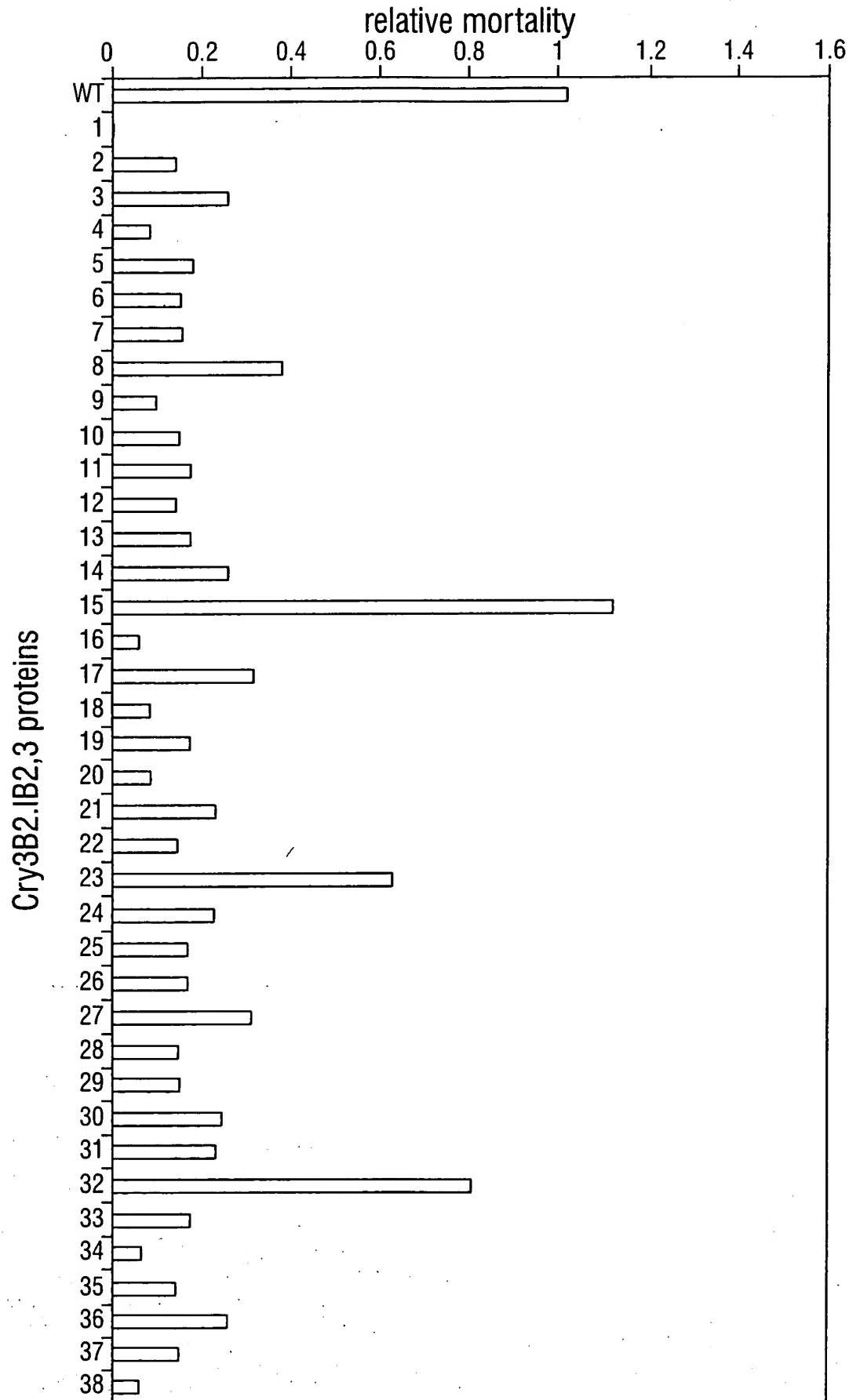


FIG. 14

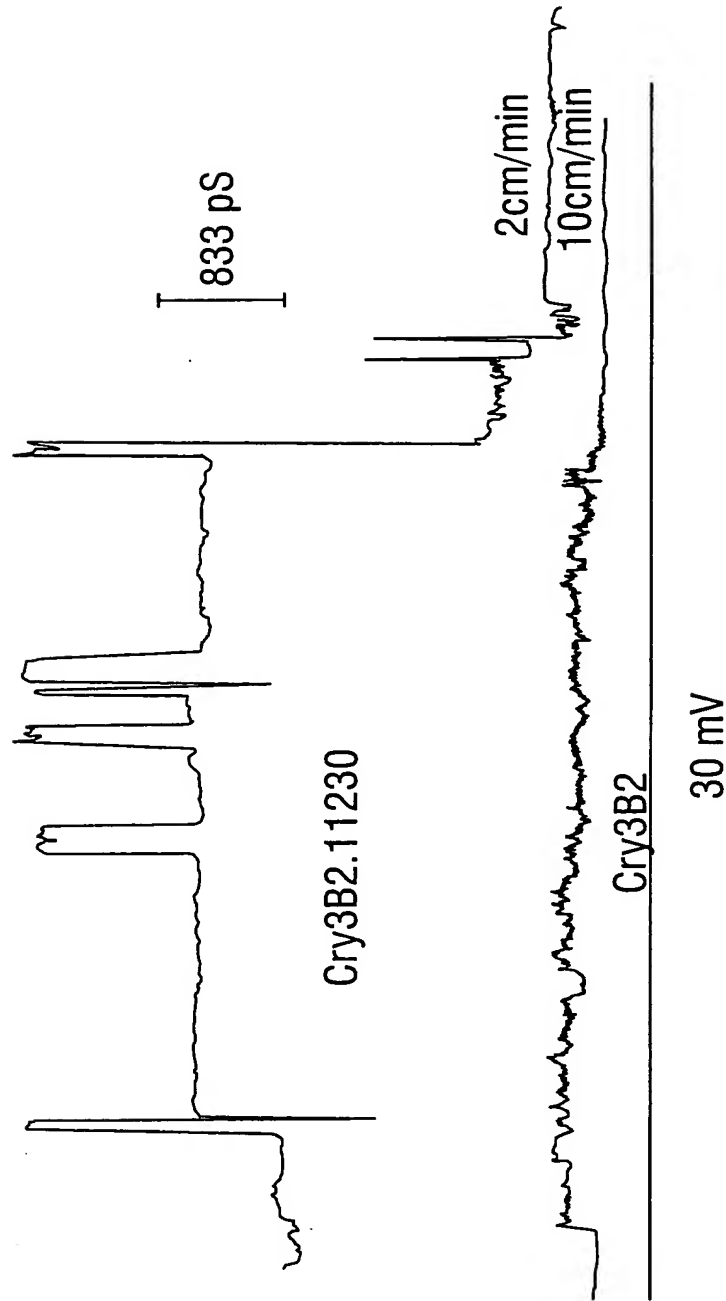


FIG. 15

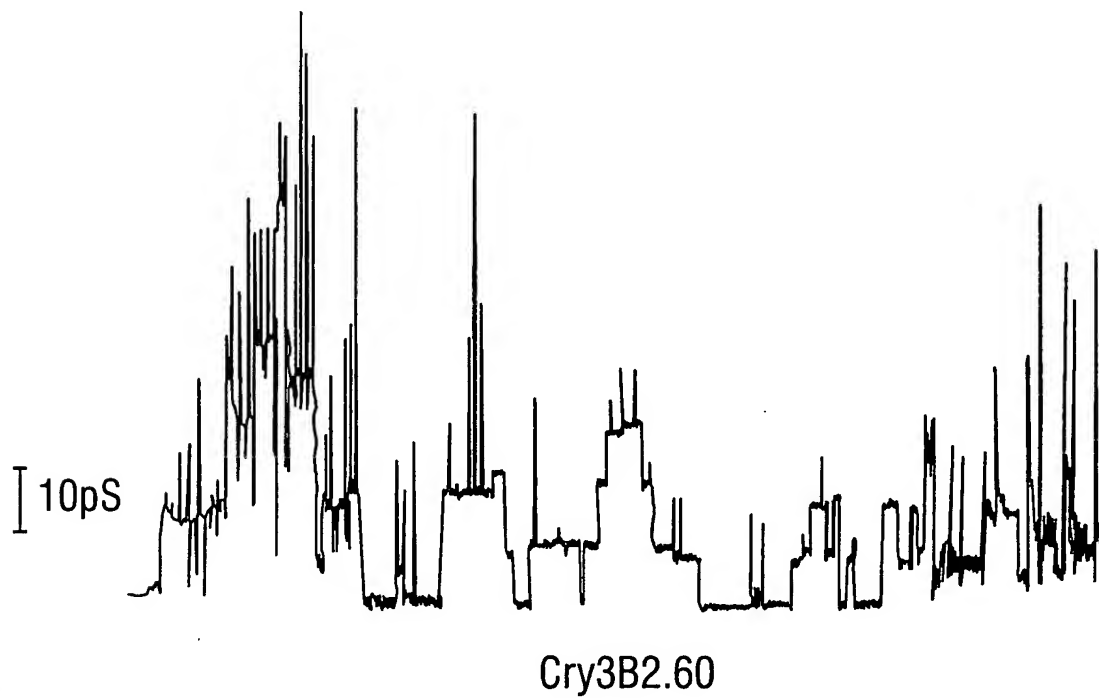
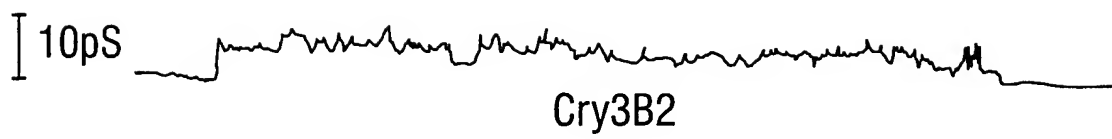


FIG. 16

ALIGNMENT OF CRY3 SEQUENCES

(Numbered according to Cry3BB)

(alpha helices underlined, beta sheets marked with + + +'s)

	1	10	20	30	40
CRY3C:	MNPNNRSEHDTIKATENNEVSNNHAQYPLADTP	-	-	TLEELNY	
CRYCBB2:	MNPNNRSEHDTIKVTPNSELPTNHNQYPLADNP	NSTLEELNY			
CRY3BB:	MNPNNRSEHDTIKVTPNSELQTNHNQYPLADNP	NSTLEELNY			
CRY3BA:	MIRMGGRKMNPNNRSEYDTIKVTPNSELPTNHNQYPLADNP	NSTLEELNY			
CRY3A:	MIRKGGRKMNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLED	LN			

	50	60	70	80	90
CRY3C:	KEFLRRTTDNNVEALDSSTTKDAIQKGISIIGDLLGVVGF	FPYGGALVSFY			
CRYCBB2:	KEFLRMTEDSSTEVLNDSTVKDAVGTGISVVGQILGVVGV	PFAGALTSFY			
CRY3BB:	KEFLRMTEDSSTEVLNDSTVKDAVGTGISVVGQILGVVGV	PFAGALTSFY			
CRY3BA:	KEFLRMADNSTEVLDSSTVKDAVGTGISVVGQILGVVGV	PFAGALTSFY			
CRY3A:	KEFLRMADNNTALDSSTTKDVIQKGISVVGDLLGVVGF	PFGGALVSFY			

	100	110	120	130	140
CRY3C:	TNLLNTIWPGE-DPLKAFMQQVEALIDQKIADYAKDKATAELQGLKNVFK				
CRY3BB2:	QSFLDTIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAE	LQGLQNNFE			
CRY3BB:	QSFLNTIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAE	LQGLQNNFE			
CRY3BA:	QSFLNAIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAE	LQGLQNNFE			
CRY3A:	<u>TNFLNTIWPSE-DPWKAFMEQVEALMDQKIADYAKNKALAE</u>	<u>LQGLQNNVE</u>			

	150	160	170	180	190
CRY3C:	DYVSALDSWDKTPLTLRDGRSQGRIRELFSQAESHFRRSMPSFAVSGYEV				
CRY3BB2:	DYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEV				
CRY3BB:	DYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEV				
CRY3BA:	DYVNALDSWKKAPVNLRSRRSQDRIRELFSQAESHFRNSMPSFAVSKFEV				
CRY3A:	<u>DYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEV</u>				

FIG. 17A

	200	210	220	230	240
CRY3C:	LFLPTYAQAANTHLLLLKDAQIYGTDWGYSTDDLNEFHTKQKDLTIEYTN				
CRY3BB2:	LFLPTYAQAANTHLLLLKDAQVFGEEWGYSSDVAEFYHRQLKLTQQYTD				
CRY3BB:	LFLPTYAQAANTHLLLLKDAQVFGEEWGYSSDVAEFYHRQLKLTQQYTD				
CRY3BA:	LFLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDIAEFYQRQLKLTQQYTD				
CRY3A:	<u>LFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYTD</u>				

	250	260	270	280	290
CRY3C:	HCAKWYKAGLDKLRGSTYEEWVKFNRYRREMTLTVLDLITLFPYDVRTY				
CRY3BB2:	HCVNWYNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFYDVRLY				
CRY3BB:	HCVNWYNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFYDIRLY				
CRY3BA:	HCVNWYNVGLNSLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFYDVRLY				
CRY3A:	<u>HCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPYDVRLY</u>				

	300	310	320	330	340
CRY3C:	TKGVKTELTRDVLTDPIVAVNNMNGYGTTFFSNIENYIRKPHLFDYLHAIQ				
CRY3BB2:	SKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLGQIE				
CRY3BB:	SKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLGQIE				
CRY3BA:	SKGVKTELTRDIFTDPIFTLNLQEYGPTFSSIENSIRKPHLFDYLRGIE				
CRY3A:	PKEVKTELTRDVLTDPIVGNNLRGYGTTF <u>FSNIENY</u> IRKPHLFDYLRHIQ				
	+++++				++++

	350	360	370	380	390
CRY3C:	FHSRLQPGYFGTDSFNYWSGNYVSTRSSIGSDEIIRSPFYGNKSTLDVQN				
CRY3BB2:	FHTRLQPGYSGKDSFNYWSGNYVETRPSIGSSKITITSPFYGDKSTEPVQK				
CRY3BB:	FHTRLQPGYFGKDSFNYWSGNYVETRPSIGSSKITITSPFYGDKSTEPVQK				
CRY3BA:	FHTRLRPGYSGKDSFNYWSGNYVETRPSIGSNDTITSPFYGDKSIEPIQK				
CRY3A:	FHTRFQPGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPQN				
	+++++	+++++	+++++	+++++	+++

	400	410	420	430
CRY3C:	LEFNGEKVFRAVANGNLAVWPVGTGGTKIHSGVTKVQFSQYNDRKDEVRT			
CRY3BB2:	LSFDGQKVYRTIANTDVAAWPNG----KIYFGVTKVDFSQYDDQKNETST			
CRY3BB:	LSFDGQKVYRTIANTDVAAWPNG----KVYLGVTKVDFSQYDDQKNETST			
CRY3BA:	LSFDGQKVYRTIANTDIAAFPDG----KIYFGVTKVDFSQYDDQKNETST			
CRY3A:	LEFNGEKVYRAVANTNLAVWPSA-----VYSGVTKVEFSQYNDQTDEAST			
	+++	+++++	++++	+++++

FIG. 17B

	440	450	460	470	480
CRY3C:	QTYDSKRNVGGIV-FDSIDQLPPITTDSELEKAYSHQLNRYVRCFLLQGG				
CRY3BB2:	QTYDSKRNNHVGGAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR				
CRY3BB:	QTYDSKRNNHVSQAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR				
CRY3BA:	QTYDSKRYNGYLGAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR				
CRY3A:	QTYDSKRNVGAVS-WDSIDQLPPETTDEPLEKGYSHQLNRYVMCFLMQGSR				
	++++	+++++			++++++

	490	500	510	520	530
CRY3C:	GIIPVFTWTHKSVDFYNTLDSEKITQIPFVKAFILVNSTSVVAGPGFTGG				
CRY3BB2:	GTIPFFTWTTHRSVDFNTIDAELITQLPVVKAYALSSGASIIIEGPGFTGG				
CRY3BB:	GTIPFFTWTTHRSVDFNTIDAELITQLPVVKAYALSSGASIIIEGPGFTGG				
CRY3BA:	GTIPFFTWTTHRSVDFNTIDAELITQLPVVKAYALSSGASIIIEGPGFTGG				
CRY3A:	GTIPVLTWTHKSVDFNMDSKKITQLPLVKAYKLQSGASVVAGPRFTGG				
	++++++	+++++	++++		++++++

	540	550	560	570	580
CRY3C:	DII-KCT-NGSGLTLYVTPAPDLTYSKTYKIRIRYASTSQVRFGIDLGSY				
CRY3BB2:	NLLFLKESSNSIAKFKVTL-NSAALLQRYRVIRIRYASTTNLRLRFVQNSNN				
CRY3BB:	NLLFLKESSNSIAKFKVTL-NSAALLQRYRVIRIRYASTTNLRLRFVQNSNN				
CRY3BA:	NLLFLKESSNSIAKFKVTL-NSAALLQRYRVIRIRYASTTNLRLRFVQNSNN				
CRY3A:	DII-QCTENGSAATIIYVTPD--VSYSQKYRARIHYASTSQITFTLSLDGA				
	++++++	++++++	+++++	+++++	+++++

	590	600	610	620	630
CRY3C:	THSISYFDKTMKGNLTLYNSFNLSSVSRPIEISG-GNKIGVSVGGIGSG				
CRY3BB2:	DFIVIIYINKTMNIDDDLTYYQTFDLATTNSNMGFSGDTNELIIGAESFVSN				
CRY3BB:	DFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN				
CRY3BA:	DFLVIYINKTMNIDGDLTYQTFDFATSNSNMGFSGDTNDFIIGAESFVSN				
CRY3A:	PFNQYFDDKTINKGDLTYNSFNLASFSTPFELSG--NNLQIGVTGLSAG				
	++++++	+++++	+++++	+++++	+++++

	640	650
CRY3C:	DEVYIDKIEFIPMD	(SEQ ID NO:109)
CRY3BB2:	EKIYIDKIEFIPVQL	(SEQ ID NO:110)
CRY3BB:	EKIYIDKIEFIPVQL	(SEQ ID NO:111)
CRY3BA:	EKIYIDKIEFIPVQ	(SEQ ID NO:112)
CRY3A:	DKVYIDKIEFIPVN	(SEQ ID NO:113)
	+++++	

FIG. 17C